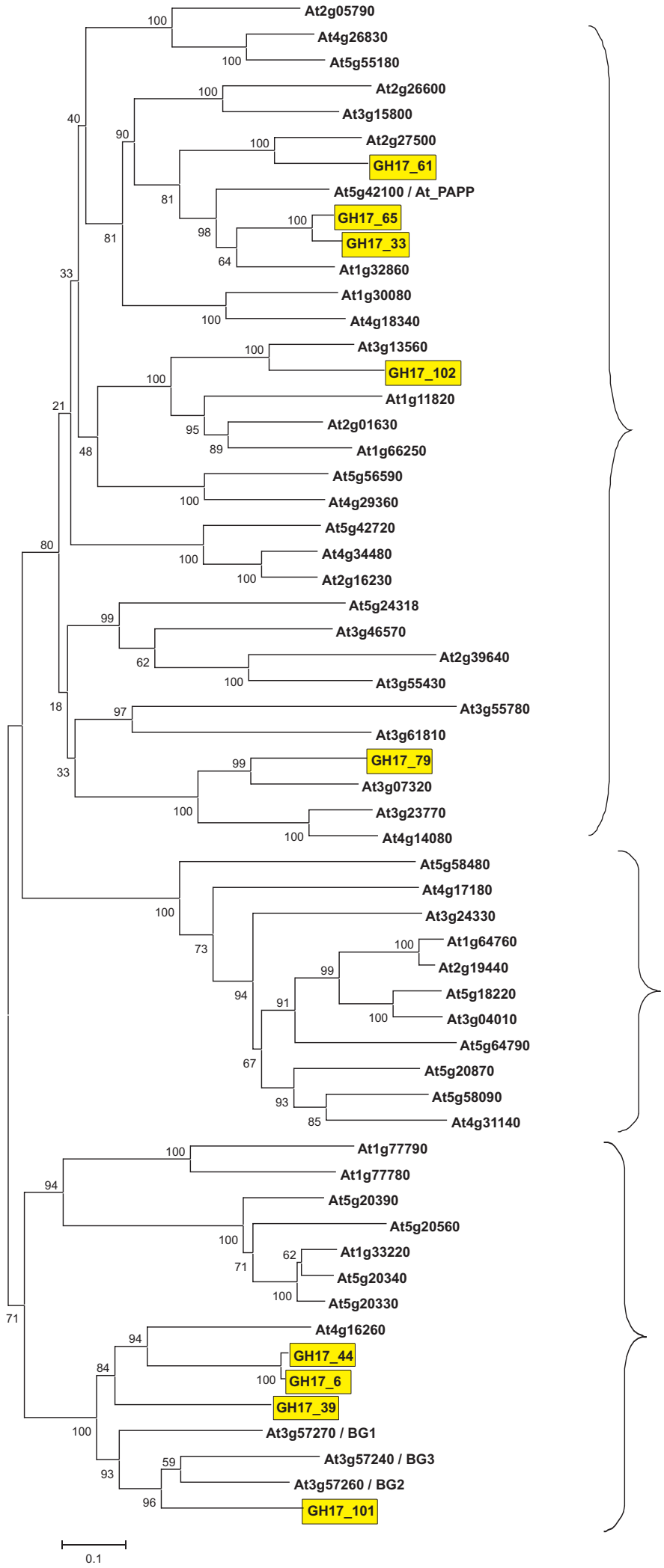
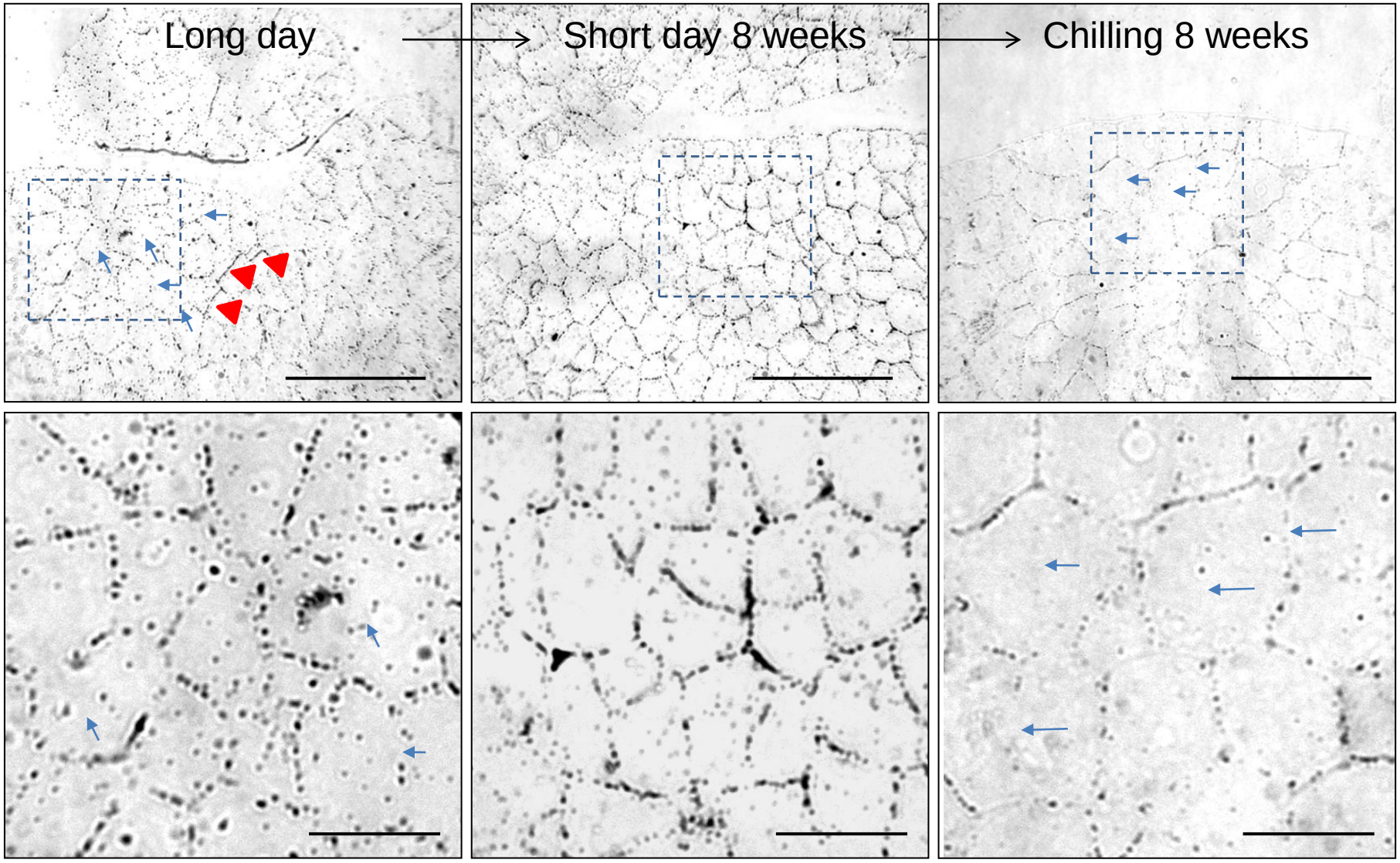
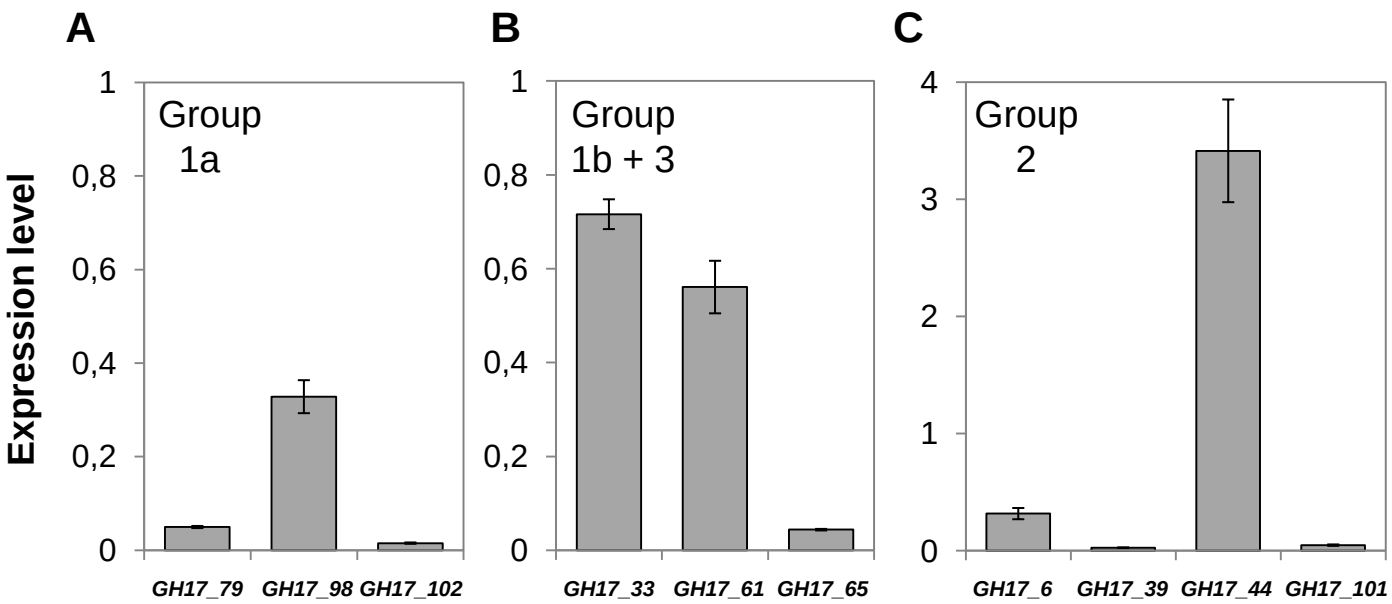

At2g05790
At4g26830
At5g55180
At2g26600
At3g15800
At2g27500
GH17_61
At5g42100 / At_PAPP
GH17_65
GH17_33
At1g32860
At1g30080
At4g18340
At3g13560
GH17_102
At1g11820
At2g01630
At1g66250
At5g56590
At4g29360
At5g42720
At4g34480
At2g16230
At5g24318
At3g46570
At2g39640
At3g55430
At3g55780
At3g61810
GH17_79
At3g07320
At3g23770
At4g14080
At5g58480
At4g17180
At3g24330
At1g64760
At2g19440
At5g18220
At3g04010
At5g64790
At5g20870
At5g58090
At4g31140
At1g77790
At1g77780
At5g20390
At5g20560
At1g33220
At5g20340
At5g20330
At4g16260
GH17_44
GH17_6
GH17_39
At3g57270 / BG1
At3g57240 / BG3
At3g57260 / BG2
GH17_101
0.1

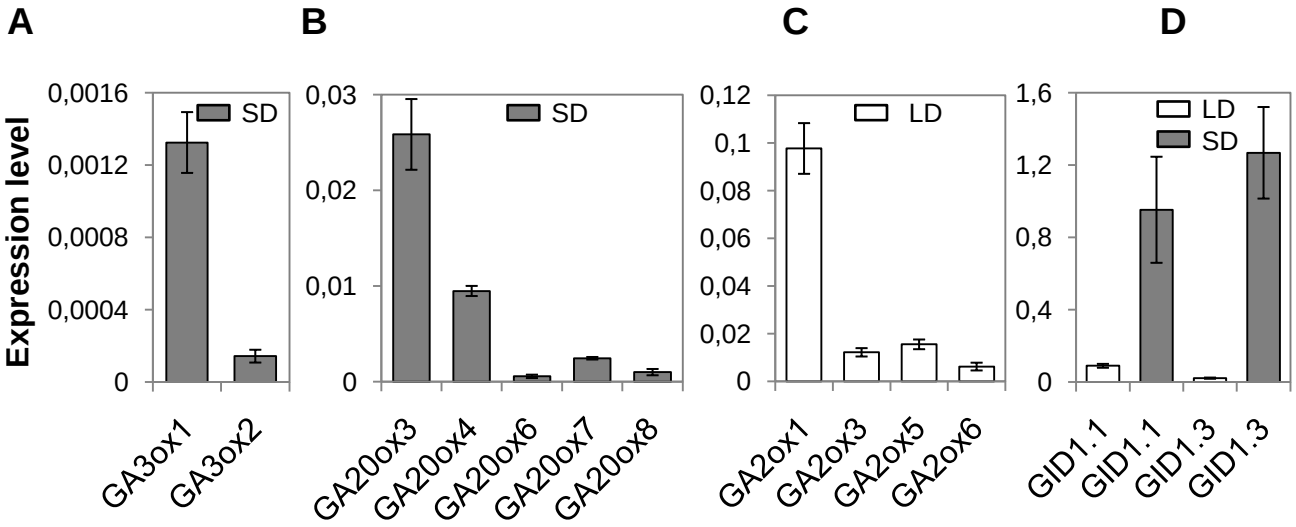
Supplemental Figure 1. Phylogenetic analysis of GH17 proteins. Analysis was performed with the full-length protein sequences of *Populus trichocarpa* and *A. thaliana* (Doxey et al., 2007). GH17 proteins were initially aligned with CLUSTAL-W and the MEGA Version 4.1 software (http://www.megasoftware.net/) was used to conduct a phylogenetic analysis based on the Neighbor Joining method on 1000 bootstrap replications. Bootstrap percentages are shown on the dendrogram branch points. *Populus* GH17 proteins are highlighted with yellow. α, β and γ refer to three major clades of *Arabidopsis* GH17 proteins (Doxey et al., 2007).


Long day
Short day 8 weeks
Chilling 8 weeks
Overview of SAM
Detail of central zone of SAM

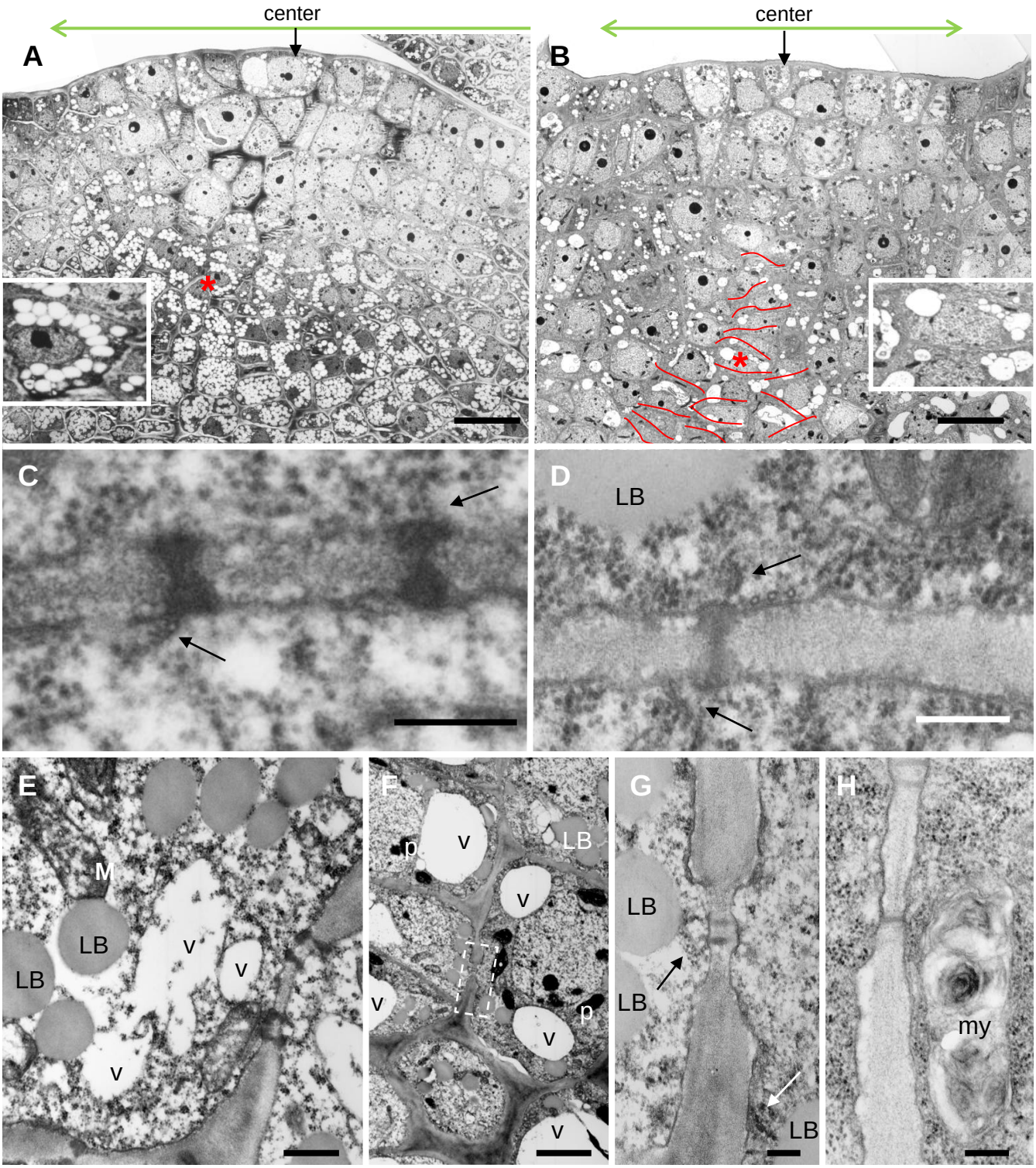
Supplemental Figure 2. Presence of callose at PD during dormancy cycling in *Populus*. Actively growing long day (LD) plants were first exposed to short days (SD) for 8 weeks to induce dormancy. Subsequently, dormancy was released by exposure to 8 weeks of chilling (grey arrows). Callose was visualized by immunolabelling with a callose-detecting polyclonal antibody, which in turn was detected with a secondary antibody-colloidal gold complex, and silver enhanced for visualization with a light microscope (Rinne et al., 2001). With this technique the number of spots and their intensity (rather than their size) is indicative of callose at PD. Part of the plasmodesmata in all meristems possess callose, but in dormant meristems (8 weeks SD), the label spots are present in practically all cell walls (middle panel), while in LD conditions and particularly in meristems released from dormancy (8 weeks chilling) label spots are less frequent and not present in all cell walls (blue arrows) creating the illusion that cells are larger than they actually are. Under LD there is continuous callose turnover, which is absent under SD, while during chilling hydrolysis of callose is predominant. Note that under LD significant amounts of callose (continuous lines) can shield off the meristem from the emerging primordium (red arrows). All pictures are from material of the same experiment treated and processed identically for labelling and photographing. Bars 50 µm (overviews) and 15 µm (details).



Supplemental Figure 3. qRT-PCR analysis of *Populus GH17* genes. **(A)** Group 1a *GH17* genes (*GH17_79*, *GH17_98* and *GH17_102*) have carbohydrate binding domain and/or GPI lipid-anchor and show highest expression level under long days and early SDs. **(B)** Group 1b (*GH17_33*, *GH17_65*) and Group 3 (*GH17_61*) *GH17* genes are GPI-anchored, putative *Arabidopsis* AtBG_ppap (At5g42100) orthologs, and are responsive to early chilling. **(C)** Group 2 (*GH17_6*, *GH17_39*, *GH17_44* and *GH17_101*) are birch lipid-body related *GH17* genes, mostly responsive to SDs and chilling. Bars represent values (± SE) normalized to actin.



Supplemental Figure 4. qRT-PCR analysis of *Populus* GA signaling genes. (**A**) and (**B**) GA biosyntheis genes *GA3-oxidases (GA3ox1* and *GA3ox2)* and *GA20-oxidases (GA20ox3*, *GA20ox4*, *GA20ox6*, *GA20ox7* and *GA20ox8).* **(C)** GA deactivating *GA2-oxidases* (*GA2ox1*, *GA2ox3*, *GA2ox5* and *GA2ox6*). **(D)** GA receptor genes (*GID1.1* and *GID1.3*). Expression levels at reference points of LDs (white bars) or SDs (grey bars) after 6 (**D**) or 8 (**A** and **B**) weeks. Bars represent values (± SE) normalized to actin.


A
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Supplemental Figure 5. TEM micrographs of GA_4-treated dormant *Populus* buds. (**A)** and **(B)** Overview of a dormant bud after exposure to 8 weeks of short day (SD) (**A**), and after subsequent 10 days feeding with GA_4 (**B**). (**A**) The dormant SAM hosts a large number of lipid bodies (LBs) in all cells. Inset shows a detail of a rib meristem (RM) cell (marked with asterisk) where LBs encircle the nucleus. (**B**) GA_4-treated buds become deficient in LBs in about 7 days, and started to form vacuoles as those depicted in the inset of a typical RM cell (marked with asterisk). Note the newly formed cell division walls at the rib meristem (RM) (marked with red lines), which has an unusually high number of cell layers, while the SAM is reduced in width (green arrows). (**C**) and (**D**) In dormant SAM PD are equipped with prominent callose-containing sphincters. (**C**) A corpus cell in the 4^{th} cell layer from the top. (**D**) Rib meristem cell. The arrows point at strands of endoplasmic reticulum (ER), that connect to PD. **(E)** L_2 layer in a control meristem (treatment with water) showed unaltered LB numbers, small vacuoles, and PD equipped with callose sphincters at day 10. (**F**) to (**H**) After 7 days GA_4-feeding buds had lost callosic-sphincters and most of their LBs, but had prominent vacuoles (v), and plastids (p). Boxed cell wall area in **(F)** is detailed in **(G),** and depicts ER strands (arrows) that connect LBs and PD. (**H**) Membranous myelin-like formations (my) might appear in LBs. Bars 10 µm (**A)** and **(B**), 500 nm (**C**) and (**E**), 200 nm (**D**), 2 µm (**F**), 100 nm (**G**) and (**H**).

Supplemental Table 1. *Populus* genes, model identifiers and primer pairs for qRT-PCR.

Enzyme/protein	Gene abbreviation	Populus trichocarpa v2.0 Locus name	Populus trichocarpa v1.1 Gene model	Primers Forward 5'-3'	Reverse 5'-3'	Reference
			Populus GH17-genes			
beta-1,3-glucanase; C-term X8	*GH17_6*	POPTR_0010s15320	fgenesh4_pm.C_LG_X000567	GTTTTGCCTGCCTTGGTAAA	AACATCACCCCTGAAAGCAC	
beta-1,3-glucanase; C-term GPI	*GH17_33*	POPTR_0001s45320	fgenesh4_pg.C_LG_I003160	CAATGCGTATCCCTTTTTCG	GGAAGTTGCTTTTCGGATCA	putative ortholog of At5g42100 (*ppap*); Levy et al. 2007a
beta-1,3-glucanase; LBP-like	*GH17_39*	POPTR_0001s26210	fgenesh1_kg.C_LG_I000076	AACCTGGGTTCAAGACAACG	CGCATCTCCAGGGTGTACTT	
beta-1,3-glucanase	*GH17_44*	POPTR_0010s15270	fgenesh1_pm.C_LG_X000469	TGCATTCTCCCCGAATAAAC	GGAAACTGTCGCGTTTTGTT	
beta-1,3-glucanase; C-term GPI	*GH17_61*	POPTR_0004s21250	eugene3.00660165	GGCTCGGGAATGAGTACCTT	AACACCTCGTTTCCGACAGT	Geisler-Lee et al. 2006
beta-1,3-glucanase; C-term GPI	*GH17_65*	POPTR_0011s15560	fgenesh4_pm.C_LG_XI000425	GCCAAATCAAGGGATTGTTG	TTGCTAATGCAGAATGCACAG	putative ortholog of At5g42100 (*ppap*); Levy et al. 2007a
beta-1,3-glucanase; C-term X8	*GH17_79*	POPTR_0002s24930	eugene3.19440001	TCAAAGACACCGACATCCAA	TTAACCCAGTGGTCCGAGAG	putative ortholog of At3g07320; Bayer et al. 2006
beta-1,3-glucanase-like; C-term X8	*GH17_98*	POPTR_0012s06720	grail3.0015000902	ATCAAAATGGCGCTTGTTTC	AAATCACAGGTGCCTTGAGC	putative ortholog of At5g61130 (PDCB1) ; Simmons et al. 2009
beta-1,3-glucanase	*GH17_101*	POPTR_0016s05800	estExt_Genewise1_v1.C_LG_XVI1825	AGAAAGGAAGCCCAAAGAGG	AGAAAGAGCCCCCAATGTTT	putative ortholog of At3g57240 (BG3); At3g57260 (BG2) (Bayer et al. 2006)
beta-1,3-glucanase; C-term X8	*GH17_102*	POPTR_0001s04360	fgenesh4_pg.C_LG_I000061+eugene3.00010060	TGCCATGAACTACCTCCACA	GGAAAGGCCTTGGGATAATG	putative ortholog of At3g13560; Bayer et al. 2006
			Populus flowering time genes			
FLOWERING LOCUS T	*FT*	POPTR_0008s07730	fgenesh4_pg.C_LG_VIII000671	GCGAGCTCAAGCCCTCTCA	TGCATCAGGGTCCACCATAAC	Böhlenius et al. 2006; Ruonala et al. 2008
CENTRORADIALIS-LIKE1	*CENL1*	POPTR_0004s21410	estExt_fgenesh4_pg.C_660171	AGTCCAACAGGAAGCAGGTTTTT	AAAGGATCTCATATCACCTCCATGAA	Böhlenius et al. 2006; Ruonala et al. 2008
CONSTANS	*CO*	POPTR_0004s10800	estExt_fgenesh4_pm.C_LG_IV0339	GATGTTGGAGTGGTGCCAGAA	TGGATAGCAGTGCTGGAGAAAAG	Ruonala et al. 2008
			Populus gibberellin biosynthesis, catabolism and signaling genes			
GA3 oxidase 1	*GA3ox1*	POPTR_0001s17680	eugene3.00011087	TGGCTCTCCTCTTGAGCATT	AACCATGTCAACCTCCTTGC	
GA3 oxidase 2	*GA3ox2*/ Ptt *GA3ox1*	POPTR_0003s05610	fgenesh4_pg.C_LG_III000353	CCCTATCTCGCTCAATCTTTCC	AGTCAAGGTGCTTTTGGTGTAG	AY433958, Israelsson et al. 2005
GA 20 oxidase 3	*GA20ox3*	POPTR_0005s20660	estExt_fgenesh4_pm.C_LG_V0384	TCGGATCTCGTTGTGCTAGA	AGTTCCAATATGGCGAAGGA	
GA 20 oxidase 6	*GA20ox6*	POPTR_0012s14040	fgenesh4_pg.C_LG_XII001220	ATTTCGACGCTTTTGTCGTT	GAGATTTTCTTGGCGTTTGG	
GA 20 oxidase 7	*GA20ox7*	POPTR_0014s06960	fgenesh4_pm.C_LG_XIV000079	ATGGCACTCCGTTACTCCTG	CCACTGCTCTATGCAAGCAA	
GA 20 oxidase 8	*GA20ox8*/ Ptt *GA20ox1*	POPTR_0015s14030	estExt_fgenesh4_pg.C_LG_XV1053	ATCAAAACCATGCCATCCA	TGGTGTCGAAGAACTTGTGC	
GA2 oxidase 1	*GA2ox1*/ Ptt *GA2ox2*	POPTR_0001s38760	eugene3.00012757	TTCTTCTCATTACCGCTCTCTG	TCTACCCAGCCCACATCAC	BU877509; Israelsson et al. 2005
GA2 oxidase 2	*GA2ox2*	POPTR_0002s19260	gw1.II.529.1	TGCCTTCCAGGTTTTAACGA	GGCAAGACCAGCTGTGGAG	
GA2 oxidase 3	*GA2ox3*	POPTR_0004s06380	fgenesh4_pg.C_LG_IV000327	GGACCTCCTAACCCTTTTGG	TGGGTTTTCCTGAAAAATGG	
GA2 oxidase 4	*GA2ox4*	POPTR_0008s10100	fgenesh4_pg.C_LG_VIII000899	AGGTAGGGTTCGGAGAGCAT	GGTAGCGGGATCAGGTGTTA	
GA2 oxidase 5	*GA2ox5*/ Ptt *GA2ox1*	POPTR_0010s15950	estExt_Genewise1_v1.C_LG_X0681	AATGGCCTATTTTGCTGCAC	TATCTCCAAGTCGCAGAGCA	
GA2 oxidase 6	*GA2ox6*	POPTR_0011s09770	estExt_fgenesh4_pg.C_LG_XI0670	CAAGCCAGCACTTCAACAGT	ATTCCTCACATGCCTTGACC	
GIBBERELLIN INSENSITIVE DWARF1	*GID1.1*	POPTR_0005s04240	estExt_fgenesh4_pg.C_700172	ACCGTGGGACTAGCCTTCTT	ACAACCTCCGAGTTGACAGG	Mauriat and Moriz 2009
GIBBERELLIN INSENSITIVE DWARF1	*GID1.3*	POPTR_0014s13170	estExt_Genewise1_v1.C_LG_XIV2782	GATCATGTTGATCGCACCAC	GTGCTCAAGGGCTTTTCAAG	Mauriat and Moriz 2009
DELLA-like1	*DELLA-like1*	POPTR_645273	grail3.0021009801	GCAAGTCGAGTCCACGTTATC	AATTCCCGTCAGCCGAAATG	BU815161; Israelsson et al. 2005
GIBBERELLIN INDUCIBLE PROTEIN-like1	*GIP-like1*	POPTR_668570	grail3.0059004501	TGGACCTGGGAGTCTCAAG	GGAACGCAGAGGCACTTC	AI166057; Israelsson et al. 2005
			Populus actin gene			
ACTIN	*ACT*	POPTR_0001s31700	estExt_fgenesh4_kg.C_LG_I0082	CGATGCCGAGGATATTCAAC	ACCAGTGTGTCTTGGTCTACCC	Ruonala et al. 2008

Supplemental Table 2. Primers for GH17 vector construction. Vectors encode eGFP-fusion proteins with *Populus* lipid body-related GH17_44 and GH17_101, and plasmodesmata-related GH17_61 and GH17_65.

Primer name	Primer sequence (5'-3')
GH17_44*att*B1	AAAAAGCAGGCTTCATGGCTAGCTTTTCCTCAA
GH17_44*att*B2	AGAAAGCTGGGTCCATATCACTCTTAAGGGAAACTG
GH17_101*att*B1	AAAAAGCAGGCTTCATGGCTAGATCAAATATAGCTG
GH17_101*att*B2	AGAAAGCTGGGTCGCGGAGATTGATGTTATATT
*att*B1-adapter	GGGGACAAGTTTGTACAAAAAAGCAGGCT
*att*B2-adapter	GGGGACCACTTTGTACAAGAAAGCTGGGT
eGFP-for	GGCCGGCCTGGAGGTGGAGGTGGAGCTGTGAGCAAGGGCG
eGFP-rev	GGCCCCAGCGGCCGCAGCAGCACCAGCAGGATCCTTGTACAGCTCGTCCA
GH17_61-P1	GCTCGATCCACCTAGGCTTCATGGCCACCTGCTTTGTTC
GH17_61-P2	CACAGCTCCACCTCCACCTCCAGGCCGGCCCAATCCACTGTTGTAAACTGG
GH17_61-P3	TGCTGGTGCTGCTGCGGCCGCTGGGGCCCAGGGCTATCTTCCTGGA
GH17_61-P4	CGTAGCGAGACCACAGGACTCAGGTGATCTGAAGTACGGA
GH17_65-P1	GCTCGATCCACCTAGGCTTCATGGAGTTCAGTAGATTTTACTACT
GH17_65-P2	CACAGCTCCACCTCCACCTCCAGGCCGGCCATAGCCATTTGAAGAACTATCC
GH17_65-P3	TGCTGGTGCTGCTGCGGCCGCTGGGGCCCTGTCAATTTCTGCTGCTGTA
GH17_65-P4	CGTAGCGAGACCACAGGACTCAAAATGCTAGTCTAAAGGC
TT-GW-for	GGGGACAAGTTTGTACAAAAAAGCAGGCTGCTCGATCCACCTAGGCT
TT-GW-rev	GGGGACCACTTTGTACAAGAAAGCTGGGTCGTAGCGAGACCACAGGA